



FIGURE 5A

SGUS -----MLYPINTETRGVFDLNGVWNFKLDYG-----KGLEEKWYESKLTDT---ISMAMP 47
HGUS LGLQGMLYPQESPSRECKELDGLWSFRADFSNRRRGFEQWYRRPLWESGPTVDMPVP 60
EGUS -----MLRPVETPTREIKKLDGLWAFSLDREN-----CGIDQRWESALQESR---AIAVP 48

SGUS SSYNDIGVTKEIRNHIGYVWYEREFVTPAYLKD---QRIVLRFGSATHKAI VV VNGELVV 104
HGUS SSFNDISQDWRLRHFVGVWYEREREVILPERWTQDLRTRVVLRI GSAHSYAI VV VNGVDTL 120
EGUS GSFNDQFADADIRNYAGNVWYQREVFI PKGWAG---QRIVLRFDA VTHYGVVWVNNQEV 105

GUS EHKGGFLPFEAEINNSLRDG---MNRVTVAVDNILDSTLPVG-LYSERHEEGLGKVIR 159
HGUS EHEGGYLPFEADISNLVQVGPLPSRLRITIAINNTLTPTTLPPTI QYLTDTSKYPKGYF 180
EGUS EHQGGYTPFEADVTPYVIAG---KSVRITVCVNNELNWQTI PPG---MVI TDENGKKK--- 157

SGUS -NKP NFDFFN YAGLHRPVKIYTTPTTYVEDISVVTDFNGPT--GTVTYTVDFQG-KAETV 215
HGUS VQNTYFDFFN YAGLQRSVLLYTTPTTYIDDI TVTTSVEQDS--GLVNYQISVKGSNLFKL 238
EGUS -QSYFHDFFN YAGIHRSVMLYTTPTNTWVDDITVVTHVAQDCN HASVDWQVVANG---DV 212

SGUS KVSVDDEEGKVVA STEGLSGNVEIPNVILWEP-----LNTYLYQIKVELVNDGLT---ID 267
HGUS EVRLLDAENKV VANGTG TQGQLKVPGVSLWWPYLMHERPAYLYSLEVQLTAQTS LGPVSD 298
EGUS SVELRDADQQV VATGQTS GTLQVVNPHLWQP-----GEGYLYELCVTAKSQTEC---D 263

SGUS VYEEPFVGVRTVEVNDGKFLINNKPFFYFKGFGKHEDTPINGRGFNEASNVMDFN ILKWIGA 327
HGUS FYTLPVGIRTVAVTKSQFLINGKPPFYFHGVNKHEDADIRGKGFDWPLL VKDFNLLRWLGA 358
EGUS IYPLRVGIRSVAVKGEQFLINHKKPPFYFTGGRHEDADLRGKGFDNVLMVHDHALMDWIGA 323

SGUS NSFRTAHYPYSEELMR LADREGLVVIDETPAVGVLHNFMA TTGLGEGSERVSTWEKIR-- 385
HGUS NAFRTSHYPYAEEMQMCDRYGIVVIDECPGVGLAL-----P-----QFFNNV 401
EGUS NSYRTSHYPYAEEMLDWADEHGIVVIDETA AVGFNLSL GIGFEAGNKP KELYSEEAVNGE 383

SGUS TFEHHQDVLRELVS RDKNHPSVVMWSIANEAATEEGAYEYFKPLVELTKELDPQKRPVT 445
HGUS SLHHMQVMEEVVR RDKNHPAVVMWSVANEPASHLESAGYYLKMVIAHTKS LDPS-RPVT 460
EGUS TQQAHLQAI KELIARDKNHPSVVMWSIANEPDTRPQGAREYFAPLAEATRKL DPT-RPIT 442

FIGURE 5B

SGUS IVLFVMA TPETDKVAELIDVIALNRYNGWYFDGGDLEAAKVHLRQEFFHAWNKRCPGKPIM 505
HGUS FVS--NSNYAADKGAPYVDVICLSYYSWYHDYGHLELIQLQLATQFENWYKKYQ-KPII 517
EGUS CVNVMFCDAHTDTISDLFDVLCNRYYGWYVQSGDLETAEKVLEKELLAWQEKLH-QPII 501

SGUS ITEYGADTVAGFHDIDPVMFTEEYQVEYYQANHVVFD--EFENFVGEQAWNFAFATSQG 563
HGUS QSEYGAETIAGFHQDPPPLMFTEEYQKSLLQYHLGLDQKRRKYVVGELIWNFAFMTEQS 577
EGUS ITEYGVDTLAGLHSMYTDMWSEYQCAWLDMYHRVFD--RVSAVVGEQVWNFAFATSQG 559

SGUS VMRVQGNKKGVFTRDRKPKLAHVFRERWTNIPDFGYKN----- 602
HGUS PTRVLGNKKGIFTRQRQPKSA AFLLRERYWKIAN-ET----- 613
EGUS ILRVGGNKKGIFTRDRKPKSA AFLLQKRWTGMNFGKPKQGGKQ 603

FIGURE 5C

Staphylococcus:	MVDLTSLYPINTETRGVFDLNGVWNFKLDYG-KGLEEKWYESKLTDTISMAMPSSY	:	55
Staph homi	-----	:	-
Staph warn	---LXLLHPI TTGTRGGFALYGXXNMLLDYG-XGLTDTWTXSLLTELSRLVVLSWT	:	52
Thermotoga	-----MVRPQRNKKRFILILNGVWNLEVTSK-----D-RPIAVPGSW	:	36
Enb/Salmon	-----	:	-
E coli	-----MLRPVETPTREIKKLDGLWAFSLDRENCGIDQRWWESALQESRAIAVPGSF	:	51
Staphylococcus:	NDIGVTKEIRNHIGYVWYEREFVPAYLKDQR--IVLRFGSATHKAI VYVNGELVV	:	109
Staph homi	-----	:	-
Staph warn	THX-LTGEX-PAISILWPNSELTVSXLXGSLXSSSLCSSLTXHVVICQXVTLXV	:	106
Thermotoga	NEQ--YQDLCYEEGPFTYKTTFFVVPKXLSQKH--IRLYFAAVNTDCEVFLNGEKVG	:	88
Enb/Salmon	-----	:	-
E coli	NDQFADADIRNYAGNVWYQREVFIPKGWAGQR--IVLRFDAVTHYGKVWVNNQEV	:	105
Staphylococcus:	EHKGGFLPFEAEIN-NSLRDGMNRVTVAVDNILLDDSTLPVGLYSERHEEGLGKVIR	:	164
Staph homi	-----	:	-
Staph warn	DHTGLIXXFEFMSTTCCXXDELVTGTLAX--ILYHXILPHGLYRKRHEXGLGKXNF	:	160
Thermotoga	ENHIEYLPFEVDVTGKVKSGENELRVVVEN-RLKVGGFPSKVPDSTGHTVGVFFGSF	:	143
Enb/Salmon	-----	:	-
E coli	EHQGGYTPFEADVTPYVIAGKSVRITVCVNNELNWQTIPPGMVIDENG-----KKK	:	157
Staphylococcus:	NKPNFDFFNAGLHRPVKIYTTPFTYVEDISVVTDFNGP--TGTVTYTVDFQGKA	:	217
Staph homi	-----	:	-
Staph warn	YXLHFAFFXYAXLXRTVXMYX-NLVRXQDI-VVTX-HX-----XX-TVEQCVXXN-	:	206
Thermotoga	PPANFDFFPYGGIIRPVLIEFTDHARILDIWVDTSESEPEKKLGKVVKIEVSEEA	:	199
Enb/Salmon	-----GKLSPTPTAYIQDVTVXTDVLN---TEQATVLGNVGADG	:	37
E coli	QSYFHDFFNAGIHRSVMLYTTPTNTWVDDITVVTHVAQD---CNHASVDWQVVANG	:	210

FIGURE 5D

Staphylococcus:	ET--VKVSVVDEEGKVVA	STEGLSGNVEI	PNVILWEPLNTLYQIKVELVNDGLTI	:	271	
Staph homi :	-----	GLSGNVEI	PNVILWEPLNTLYQIKVELVNDGLTI	:	35	
Staph warn :	KIXSVKITILDENDHAI	XESEGAKGNVTIQNPILWQPLHAYLYNMKVLELLNDNECV		:	262	
Thermotoga :	VGQEMTIKLGEEEKKIRTS	NRFFVEGEFIIENARFWSLEDPLYPLKVELEKD----		:	251	
Enb/Salmon :	D---IRVELRDGQQQI	VAQGLGATGIFELDNPHLWEPGEGYLYELRVTC	EAN-GEC	:	89	
E coli :	D---VSVELRDADQ	QVVATGQTSGLQVVNPHLWQPGEGYLYELCVTAKSQ-TEC		:	262	
Staphylococcus:	DVYEEPF	GVRTVEVNDGKFLINN	KPFYFKGFGKHEDTPINGRGFNEASNVMDFNII	:	327	
Staph homi :	DVYEEPF	GVRTVEVNDGKFLINN	KPFYFKGFGKHEDTPINGRGFNEASNVMDFNII	:	91	
Staph warn :	DYTERFGIR	SVVEVKDGGQLINDKPFYFKGFGKHEDTY-NGRGLNESANVMDINLM		:	317	
Thermotoga :	-EYTLDIGIR	TISWDEKRLYLNGKPVFLKGFGKHEEFVLGQGTFFYPLMIKDFNLL		:	306	
Enb/Salmon :	DEYPVRVGIR	SITXKGEQFLINH	KPFYLTGFGRHEDADFRGKGFD	PVLMVHDHALM	145	
E coli :	DIYPLRVGIR	SVAVKGEQFLINH	KPFYFTGFGRHEDADLRGKGFD	NVLMVHDHALM	318	
Staphylococcus:	KWIGANSFRTAHYPYSEEL	MRLLADREGLVVIDETPAVG	VH-LNFMATTGLGEGSER	:	382	
Staph homi :	KWIGANSFRTAHYPYSEEL	MRLLADREGLVVIDETPAVG	VH-LNFMATTGLGEGSER	:	146	
Staph warn :	KWIGANSFRTSHYPYSEEM	MRLLADEQGI	VVIDETTXVGIH-LNFMXTLGSX---	A	369	
Thermotoga :	KWINANSFRTSHYPYSEEW	LDLADRLGILVIDEAPHVGIT-----	R---Y	:	348	
Enb/Salmon :	NWIGANSYRTSHYPYAEK	MLDWADEHVI	VVINETAAGGFNTLSLGITFDAGERPKE	:	201	
E coli :	DWIGANSYRTSHYPYAEEM	MLDWADEHGI	VVIDETA	AVGFN-LSLGIGFEAGNKPKE	373	
Staphylococcus:	VSTWEKIR	TFE--HHQDVLREL	VS	RDKNHPSVVMWSIANEAA	TEEEGAYEYFKPL	435
Staph homi :	VSTWEKIR	TFE--HHQDVLREL	VS	RDKNHPSVVMWSIANEAA	TEEEGAYEYFKPL	199
Staph warn :	HDTWXEF	DTLE--FHKEVI	XDLI	XRDKNHAWVMWXFGNEXGXNKGKAKAXFE	PF	422
Thermotoga :	HYNPETQ	KIAE-----	DNIRRMIDRHKNHPSVIMWSV	ANEPESNHPDAEGFFKAL		398
Enb/Salmon :	LYSEEA	INGETSQQAHLQAI	KELI	ARDKNHPSVVCWSIANEPDTRPN	GAREYFAPL	257
E coli :	LYSEEA	VNGET-QQAHLQAI	KELI	ARDKNHPSVVMWSIANEPDTRPQ	GAREYFAPL	428

FIGURE 5E

Staphylococcus:	VELTKELDPQKRPVTIVLFVMA--PETDKVAELIDVIALNRYNGWYFDGGDLEAA	: 489
Staph homi	: GGAAKELDPXKRPVTIVLFVMA--PETDKVAELIDVIALNRYNGWYFDGGDLEAA	: 253
Staph warn	: VNLAGKDXXXXPVTIVTILXAX--RNVCEVXDLVDVCLXXXGWYXQSGDLEGA	: 476
Thermotoga	: YETANEMDR-TRPVVMVSMMDAPDERTRDVALKYFDIVCVNRYYGWYIYQGRIEEG	: 453
Enb/Salmon	: AKATRELDP-TRPITCVNVMFCD--AESDTITDLFDVVCLNRYYGWYVQSGDLEKA	: 310
E coli	: AEATRKLDP-TRPITCVNVMFCD--AHTDTISDLFDVLCNRYYGWYVQSGDLETA	: 481
Staphylococcus:	KVHLRQEFHAWNKRCPGKPIMITEYGADTVAGFHDIDPVMFTTEEQVEYYQANHVV	: 545
Staph homi	: KVHLRQEFHAWNKRCPGKPIMITEYGADTVAGFHDIDPVMFTTEEQVEYYQANHVV	: 309
Staph warn	: KXALDKEXXEWKXQXNKPXMFTEYGVDXVVGGLXXXPDKMXPEEYKMXFYKGYXKI	: 532
Thermotoga	: LQALEKDIEELYARHR-KPIFVTEFGADAIAGIHYDPPQMFSEEQAEELVEKTIRL	: 508
Enb/Salmon	: EQMLEQEQLLAWQSKLH-RPIIITEYGVDTLAGMPSPVYPPDMWSEKQYQWKWLEMYHRV	: 365
E coli	: EKVLEKELLAWQEKLH-QPIIITEYGVDTLAGLHSMYTDMMWSEEQCAWLDMYHRV	: 536
Staphylococcus:	FDEFENFVGEQAWNFAADFATSQGVMRVQGNKKGVFTRDRKPKLAHVFRERWTNIP	: 601
Staph homi	: FDEFENFVGEQAWNFAADFATSQGVMRVQGNKKGVFTRDRKPKLAHVFRERRTNIP	: 365
Staph warn	: MDK-----	: 535
Thermotoga	: LLKKDYIIIGTHVWAFADFKTPQNVRRPILNHKGVFTRDRQPKLVAHVLRRLWSEV-	: 563
Enb/Salmon	: FDRGSVC-----	: 372
E coli	: FDRVSAVVGEQVWNFAADFATSQGILRVGGNKKGIFTDRDRKPKSAFLLQKRWTGMN	: 592
Staphylococcus:	DFGYKN-----	: 607
Staph homi	: DFGYKNASHHH	: 376
Staph warn	: -----	: -
Thermotoga	: -----	: -
Enb/Salmon	: -----	: -
E coli	: FGEKPPQQGGKQ	: 603

FIGURE 5F

B psm : -----ATGGTAGATCTGACTAGT-CTGTACCCGATCAACACCGAGACCCGTGGCGTCTTCGACCTCAATGGCGTCTG : 71
Salmonella: CCNCCCNTTTTNGTANCNTNTTTGNNANCTGCTGCANNNGATCACNACNNGANNCGGGNGGGTTTCGNNCTCTATGGCNCGNG : 84
Pseudomona: ----- : -

B psm : GAACTTCAAGCTGGACTACGGGAAAGGACTGGAAGAGAAAGTGGTACGAAAGCAAGCTGACCGACACTATTAGTATGGCCGCTCCC : 155
Salmonella: GAACNNNATGNTGNCNACNGTTNANGACTGACAGACACGCTGGAGCTAAAGCTTGCTG-CCGA-ACTATCACTCAGNTCNTGNA : 166
Pseudomona: -----TGCTGGACNACNGTTNAGGATTTTAGACACGNGGAGCTAAAGCTTGCTGACCN-AACTATCACGCCGCGNCGTGCA : 75

B psm : AAGCAGTTACAATGACATTGGCGTGACCAAGGAAATCCGCAACCATATCGGATATGT-CTGGTACGAACGTGAGTTCACGGT-G : 237
Salmonella: AGTTGG--ACAAC-ACATTNCC-TGACANGNGAAAAGC-CCGCCATATCCATACTGTGCTGGCCCAACANTGAGTTCACNGTCG : 245
Pseudomona: NGCTTGG-ACCGCGACATTNCC-TGACANGNGAAANACTCCGCCATATCCATCTT-TGCTGGCCCCAACAGTGAGTTNACNGT-N : 155

B psm : CCGGCCATCTGAAGGATCAGC-GTATCGTGTCTCCGCTTCGGCTCTGCAACTCACAAAGCAATT-GTCTATGTCAATG-GTGAG : 318
Salmonella: TCGNACTNTATGANGGATCACCTGTATCGANCTCCNTTNNATNTCTNCAGCTAACATAACTGTGNGCATATGTCAATGNATGAC : 329
Pseudomona: NCGNACNNNTNNGANGGATCAGT-GNATCGAGCTCCNTTNNANNTTCTNC-GCTAACATAACATGTNGCATATGTCAATNAATNAC : 237

B psm : -CTGGTCG-TGGAGCACAAAGGGCGG--ATTCTCTGCCATTCTGAAGCGGAAATCAACAATC-GCTGCGTGATGGCATGAATCGCG : 397
Salmonella: -CTGGTCGGTGNANCACACCGGGCGGTNATTTGNTGNNATTCGAAATTTNATGTCAACAACCTTTGNTGCANGNTGGAATGAATCTGG : 412
Pseudomona: GCTGGNCG-TGGANCNCACCGGGCTNATTCGNTGNNATTCGAAATTGNAATGNCAACAACCTNTGNTGCACGNTGNAANAATTCG : 320

B psm : TCACCGTCG-CCGTGGACAACATCCTCGACGATA-GCACCCCTCCC--GGTGGGGCTGTACAGCGAGC-GCCACGAAGAGGGC-C : 475
Salmonella: GGGCCAGGACTTTGGCCANCTTCCTNAACCATTCGCANCCCTCCCCAGTGGCTTGACACNATTTG-NGCCCCCAAAAGGC-N : 494
Pseudomona: GTNACAGGACTTTGGCCN-CTTCCTAAACCATN-GCATCCTCCC--NATGGGCTGTACACGAATGNGCCCCCCCCAAANGGCNT : 399

B psm : TCGGAAAAGTCATTTCGTAACAAGCCGAAC-TTCGACTTCTTCAACTATGCAGGCCCTGCACCGTCCGGTGAAAATC-TACACGAC : 557
Salmonella: TCAGATAGG-CATTT-TGACAAAGCTCCAN-NTTAACTTTTCAACTATGCNNGNCCCTGCACCCGACGCTGAAAANGTACANGAN : 575
Pseudomona: TCAGAAAGGCAATTTNTAACAAGGCNGANNTTTGACTTTTTCAACTATGCAGNNCTGCACCCGACGCTGAAAATG-TACANGAC : 482

B psm : CCCGTTTACGTACGTCGAGGACATCTCGGTTGTGACCGACTTCAATGGCCCAACCGGACTGTGACCTATACGG--TGGACTTT : 639
Salmonella: CCT-TGTACGTTCCACCAAGANATTTAAGGTGTGACCCACNTCCATTTTCTTAACNGGACTGTGACTNATAAAGNTGACCCNTT : 658
Pseudomona: CCTGGGTACGTNACNACCAAGACATNNAAGTGTGACCGACTCCATTGTNCTAACCCGGGACTGT-ACCTATAATG--CGGACTAT : 563

B psm : CAAGGCAAAGCCGAGACCGTGAAAGTGTCCGTGATGAGGAAGGCAAGTGGTCGCAAGCACCGAGGCCCTGAGCGGTAAC : 723
Salmonella: CANGGACACATTGCAA--TGACCCCTTTNAAACGGAANAACCCCGGNTTAAAGG--AAAAACAATTTGGTTGGGNAGTCCAN : 737
Pseudomona: CANGGCAATGCATGAC--GTNGAANCACACACAGGATNAGGAAAACAANTGGT--GGNANCNCACCANGCCCATGATTGTCCAC : 643

FIGURE 5G

B psm	:	GTGGAGATTCCGAAATGTCATCCTCTCTGGGAACCACTGAACACGTAATCTCTACCAAGTGGAACTGGTGAACGACGACTG	:	807
Salmonella:		CCAAGGGCCAAATTANTTGTTCNCGGGGGANTAAANCCCCCN-----	:	779
Pseudomona:	G-----	-----	:	644